

EX. SEARCH NOTES

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 2, 2004, 21:20:01 ; Search time 1549 Seconds
(without alignments)
2602.261 Million cell

updates/sec

Title: US-09-843-377-3_COPY_1000_1092
Perfect score: 93
Sequence: 1 gagctgggagcaatccattc.....ctccagaaaacattgaggtg 93

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 1603530

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sta.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
21: em_or.*
22: em_ov.*
23: em_pat.*
24: em_ph.*
25: em_pl.*
26: em_ro.*
27: em_sta.*
28: em_un.*
29: em_vi.*
30: em_htg_hum.*
31: em_htg_inv.*
32: em_htg_other.*
33: em_htg_mus.*
34: em_htg_pln.*
35: em_htg_rnd.*
36: em_htg_mam.*
37: em_htg_vrt.*
38: em_sy.*
39: em_htgo_hum.*
40: em_htgo_mus.*
41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	
1	18.6	20.0	45	6 AR078468	AR078468	
Sequence 2	17.2	18.5	30	6 A11493	A11493	
Nucleotide 3	17	18.3	49	6 AX404630	AX404630	
Sequence 4	16.8	18.1	50	6 AX159154	AX159154	
Sequence 5	16.6	17.8	30	6 AR093240	AR093240	
Sequence c 6	16.6	17.8	34	11 C75763	C75763 Homo	
sapien c 7	16.6	17.8	39	6 I44807	I44807 Sequence	
31	8	16.6	17.8	49	6 I79331	I79331 Sequence
34	9	16.6	17.8	50	6 AR125663	AR125663
Sequence 10	16.6	17.8	50	6 I47075	I47075 Sequence	
5	c 11	16.4	17.6	47	6 AR149818	AR149818
Sequence c 12	16.4	17.6	47	6 AR289717	AR289717	
Sequence c 13	16.4	17.6	47	6 BD007169	BD007169	
Improved 14	16.4	17.6	50	6 AX159152	AX159152	
Sequence c 15	16.2	17.4	40	6 AR078049	AR078049	
Sequence						

16	16.2	17.4	47	6 AR288877	AR288877
Sequence 17	16.2	17.4	48	9 HSTCRA2J	Z28346
H.sapiens (18	16.2	17.4	48	9 S74027	S74027 TCR
alpha V c 19	16.2	17.4	50	6 AR356512	AR356512
Sequence 20	16	17.2	41	6 AX513847	AX513847
Sequence c 21	16	17.2	41	6 AX514818	AX514818
Sequence c 22	16	17.2	41	6 AX517176	AX517176
Sequence 23	16	17.2	41	6 AX517724	AX517724
Sequence c 24	16	17.2	50	6 AX199602	AX199602
Sequence c 25	16	17.2	50	9 AF044111	AF044111 Homo
sapi c 26	15.8	17.0	39	6 BD263040	BD263040
Vectors f c 27	15.8	17.0	40	6 AR127202	AR127202
Sequence c 28	15.8	17.0	40	6 BD130543	BD130543
Controlle c 29	15.8	17.0	42	6 AR109086	AR109086
Sequence c 30	15.8	17.0	42	6 AR200741	AR200741
Sequence c 31	15.8	17.0	44	6 I43354	I43354 Sequence
8 32	15.8	17.0	47	6 AR289659	AR289659
Sequence 33	15.6	16.8	27	6 AX417271	AX417271
Sequence 34	15.6	16.8	30	6 BD095102	BD095102 N-Type
ca 35	15.6	16.8	33	6 AR022050	AR022050
Sequence 36	15.6	16.8	33	6 I92840	I92840 Sequence
14 37	15.6	16.8	35	6 E27408	E27408 Process
for 38	15.6	16.8	43	6 BD190955	BD190955 DNA
methy 39	15.6	16.8	43	9 F202550S09	AF202558 Homo
sapi c 40	15.6	16.8	44	6 AX457962	AX457962
Sequence c 41	15.6	16.8	47	6 AR284775	AR284775
Sequence 42	15.6	16.8	48	6 AX805934	AX805934
Sequence 43	15.6	16.8	50	6 AX157284	AX157284
Sequence 44	15.4	16.6	25	6 AX609394	AX609394
Sequence c 45	15.4	16.6	28	6 BD141779	BD141779 Novel
G p					

ALIGNMENTS

RESULT 1
AR078468
LOCUS AR078468 45 bp DNA linear PAT 31-
AUG-2000
DEFINITION Sequence 8 from patent US 5962664.
ACCESSION AR078468
VERSION AR078468.1 GI:10005214
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 45)
Friedhoff,A.J., Basham,D.A. and Miller,J.C.
AUTHORS Psychosis protecting nucleic acid, peptides, compositions and
TITLE method of use
JOURNAL Patent: US 5962664-A 8 05-OCT-1999;
FEATURES Location/Qualifiers
source 1..45
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 20.0%; Score 18.6; DB 6; Length 45;
Best Local Similarity 84.0%; Pred. No. 4.2e+04;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 10 GCACCTCCATTCTGCGCTGGGTGACAA 34
||||||| | ||||| |||||
Db 4 GCACCTCCATCCAGCTCGGCACAA 28

RESULT 2
A11493
LOCUS A11493 30 bp DNA linear PAT 01-
DEC-1993
DEFINITION Nucleotide sequence 33 from patent number EP0170204.
ACCESSION A11493
VERSION A11493.1 GI:492477
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 30)
AUTHORS Hauptmann,R., Meindl,P., Dworkin-Rastl,E., Adolf,G.D.,
Swetly,P.,
Pieler,C. and Haevel,N.
TITLE Genetic sequences, type I interferon peptide coded by them,
and

JOURNAL these organisms producing the same
Patent: EP 0170204-A 33 05-FEB-1986;
BOEHRINGER INGELHEIM INTERNATIONAL GmbH
FEATURES Location/Qualifiers
source 1..30
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

ORIGIN

Query Match 18.5%; Score 17.2; DB 6; Length 30;
Best Local Similarity 86.4%; Pred. No. 1.4e+05;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 GGAGCACTCCATTCTGGCTGGG 28
|||||
Db 9 GGAGCACTCCATTCTGGCTGTG 30

RESULT 3

AX404630 49 bp DNA linear PAT 14-

LOCUS

JUN-2002

DEFINITION Sequence 4 from Patent W00224745.

AX404630

VERSION AX404630.1 GI:21437911

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Abken,H. and Schinkoethe,T.

TITLE Method for detecting tumor cells

JOURNAL Patent: WO 0224745-A 4 28-MAR-2002;

Abken, Hinrich (DE)

FEATURES Location/Qualifiers

source 1..49

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 18.3%; Score 17; DB 6; Length 49;
Best Local Similarity 63.4%; Pred. No. 1.8e+05;
Matches 26; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 5 TGGGAGCACTCCATTCTGCGCTGGGTGACAACTGCTTGGTTT 45
|||||
Db 2 TGGAAAACTCCACTCACTTGTTCAGAGTGGGTGGGTT 42

RESULT 4

AX159154 50 bp DNA linear PAT 22-

LOCUS

JUN-2001

DEFINITION Sequence 2482 from Patent W00140521.

AX159154

VERSION AX159154.1 GI:14540485

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Shimkets,R.A. and Leach,M.

TITLE Nucleic acids containing single nucleotide polymorphisms and

methods of use thereof

JOURNAL Patent: WO 0140521-A 2482 07-JUN-2001;

Curagen Corporation (US)

FEATURES Location/Qualifiers

source 1..50

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

misc_feature 25..26

/note="Nucleotide deleted between bases 25 and 26

Accession number cg39567412"

misc_feature 26

/note="2 of 2 allelic variants (2481 is other entry)"

ORIGIN

Query Match 18.1%; Score 16.8; DB 6; Length 50;
Best Local Similarity 61.4%; Pred. No. 2.2e+05;
Matches 27; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 37 CCTTGGTTTCAAGACTATCGGAATGTGACTGTGGGCTCCAGA 80
|||||
Db 5 CCATGGCGTGACACAGGGGACTGTCAATCACAGGCTTTCTATA 48

RESULT 5

AR093240 30 bp DNA linear PAT 08-

LOCUS

SEP-2000

DEFINITION Sequence 14 from patent US 5998697.

AR093240

VERSION AR093240.1 GI:10019990

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 30)

AUTHORS Devlin,R.H.

TITLE Transgenic fish and vectors therefor

JOURNAL Patent: US 5998697-A 14 07-DEC-1999;

FEATURES Location/Qualifiers

source 1..30

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Query Match 17.8%; Score 16.6; DB 6; Length 30;
Best Local Similarity 82.6%; Pred. No. 2.4e+05;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 17 ATTCTGCTGGGTGACAAATGCTT 39
|||||
Db 7 ATCCAGCTTCATGATGACT 29

RESULT 6

C75763/c

LOCUS C75763

FER-1999

DEFINITION

tagged

site.

ACCESSION C75763

VERSION C75763.1 GI:3176205

KEYWORDS STS; DH; Digital hybridization.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (sites)

AUTHORS Asakawa,S. and Shimizu,N.

TITLE High-fidelity digital hybridization screening

JOURNAL Genomics 49 (2), 209-217 (1998)

MEDLINE 98260670

PUBMED 9598308

REFERENCE 2 (bases 1 to 34)

AUTHORS Asakawa,S. and Shimizu,N.

TITLE Direct Submission

JOURNAL Submitted (09-SEP-1997) Shuichi Asakawa, Keio University

School of

Medicine, Department of Molecular Biology; Shinanomachi 35,

Shinjuku-ku, Tokyo 160, Japan (E-mail:asa@med.keio.ac.jp.

Tel:81-3-3351-2370)

FEATURES Location/Qualifiers

source 1..34

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 17.8%; Score 16.6; DB 11; Length 34;
Best Local Similarity 71.0%; Pred. No. 2.5e+05;
Matches 22; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 5 TGGGAGCACTCCATTCTGCGCTGGGTGACAAAT 35
|||||
Db 31 TGTGAGCTAGTCATTCAGCTGTGTAAACAT 1

RESULT 7

I44807/c

LOCUS I44807

OCT-1997

DEFINITION Sequence 31 from patent US 5635599.

ACCESSION I44807

VERSION I44807.1 GI:2469520

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 39)

AUTHORS Pastan,I.H., Kreitman,R.J. and Puri,R.K.

TITLE Fusion proteins comprising circularly permuted ligands

JOURNAL Patent: US 5635599-A 31 03-JUN-1997;

FEATURES Location/Qualifiers

source 1..39

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Query Match 17.8%; Score 16.6; DB 6; Length 39;
Best Local Similarity 71.0%; Pred. No. 2.5e+05;
Matches 22; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 43 TTTCACACTATCGGAATGTGACTGTGCGGC 73
|||||
Db 35 TCTCAACACTCACCGAGGTAACGGTGGGC 5

RESULT 8

I79331

LOCUS I79331

JUN-1998

DEFINITION Sequence 34 from patent US 5707796.

ACCESSION I79331

VERSION I79331.1 GI:3207621

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 49)

AUTHORS Gold,L. and Beutel,B.

TITLE Method for selecting nucleic acids on the basis of structure

JOURNAL Patent: US 5707796-A 34 13-JAN-1998;

FEATURES Location/Qualifiers

source 1..49

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Query Match 17.8%; Score 16.6; DB 6; Length 49;
Best Local Similarity 71.0%; Pred. No. 2.6e+05;

Matches 22; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 49 CACTATCGGAATGTGACTGTGGGCTCCAG 79
||||| ||| || ||||| ||| |||
Db 19 CACTATAGGGAGATGCTGTGAGCATGCTG 49

RESULT 9

ARI25663
LOCUS ARI25663 50 bp DNA linear PAT 16-
MAY-2001
DEFINITION Sequence 5 from patent US 6177557.
ACCESSION ARI25663
VERSION ARI25663.1 GI:14111725
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 50)
AUTHORS Janjic,N., Gold,L. and Tasset,D.
TITLE High affinity ligands of basic fibroblast growth factor and thrombin
JOURNAL Patent: US 6177557-A 5 23-JAN-2001;
FEATURES Location/Qualifiers
source 1..50
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 17.8%; Score 16.6; DB 6; Length 50;
Best Local Similarity 71.0%; Pred. No. 2.6e+05;
Matches 22; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 49 CACTATCGGAATGTGACTGTGGGCTCCAG 79
||||| ||| || ||||| ||| |||
Db 20 CACTATAGGGAGATGCTGTGAGCATGCTG 50

RESULT 10

147075
LOCUS 147075 50 bp DNA linear PAT 07-
OCT-1997
DEFINITION Sequence 5 from patent US 5639868.
ACCESSION 147075
VERSION 147075.1 GI:2471040
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 50)
AUTHORS Janjic,N. and Gold,L.
TITLE High-affinity RNA ligands for basic fibroblast growth factor
JOURNAL Patent: US 5639868-A 5 17-JUN-1997;
FEATURES Location/Qualifiers
source 1..50
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 17.8%; Score 16.6; DB 6; Length 50;
Best Local Similarity 71.0%; Pred. No. 2.6e+05;
Matches 22; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 49 CACTATCGGAATGTGACTGTGGGCTCCAG 79
||||| ||| || ||||| ||| |||
Db 20 CACTATAGGGAGATGCTGTGAGCATGCTG 50

RESULT 11

ARI149818/c
LOCUS ARI149818 47 bp DNA linear PAT 08-
AUG-2001
DEFINITION Sequence 19 from patent US 6228621.
ACCESSION ARI149818
VERSION ARI149818.1 GI:15114409
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 47)
AUTHORS Williams,W.V., Madaio,M. and Weiner,D.B.
TITLE Plasmids encoding immunogenic proteins and intracellular targeting sequences
JOURNAL Patent: US 6228621-A 19 08-MAY-2001;
FEATURES Location/Qualifiers
source 1..47
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 17.6%; Score 16.4; DB 6; Length 47;
Best Local Similarity 60.5%; Pred. No. 3.1e+05;
Matches 23; Conservative 2; Mismatches 13; Indels 0; Gaps 0;

Qy 55 CGGAATGTGACTGTGGGCTCCAGAAACATTGAGGT 92
||: ||: || || ||||| || ||||| |||
Db 46 CAGRYTGYTGACGTGGACCTCCTGATAAGATTAGAT 9

RESULT 12

AR289717/c
LOCUS AR289717 47 bp DNA linear PAT 12-
JUN-2003
DEFINITION Sequence 1452 from patent US 6537751.
ACCESSION AR289717
VERSION AR289717.1 GI:31677001
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.
REFERENCE 1 (bases 1 to 47)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 1452 25-MAR-2003;
FEATURES Location/Qualifiers
source 1..47
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 17.6%; Score 16.4; DB 6; Length 47;
Best Local Similarity 67.6%; Pred. No. 3.1e+05;
Matches 23; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 20 CTGCCTGGGTGACAAATGCTTGGTTTCAACACTA 53
||||| || ||||| ||||| |||
Db 36 CTGCTTCCCTACRTATGCTTGGTTTCCATCCTA 3

RESULT 13

BD007169/c
LOCUS BD007169 47 bp DNA linear PAT 31-
JAN-2002
DEFINITION Improved vaccines.
ACCESSION BD007169
VERSION BD007169.1 GI:18635540
KEYWORDS JP 2001503260-A/14.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 47)
AUTHORS Williams,W.V., Madaio,M. and Wehner,D.B.
TITLE Improved vaccines
JOURNAL Patent: JP 2001503260-A 14 13-MAR-2001;
COMMENT THE TRUSTEES OF THE UNIVERSITY OF PENNSYLVANIA
OS Unknown
PN JP 2001503260-A/14
PD 13-MAR-2001
PF 23-OCT-1997 JP 1998519728
FR 23-OCT-1996 US 60/029592
PI WILLIAM V WILLIAMS, MICHAEL MADAIO, DAVID B WEHNER PC
C12N15/09,A61K48/00//A61K39/00,C12N15/00
CC
FH Key Location/Qualifiers
FT source 1..47
FT /organism="Unknown".

FEATURES

source 1..47
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN

Query Match 17.6%; Score 16.4; DB 6; Length 47;
Best Local Similarity 60.5%; Pred. No. 3.1e+05;
Matches 23; Conservative 2; Mismatches 13; Indels 0; Gaps 0;

Qy 55 CGGAATGTGACTGTGGGCTCCAGAAACATTGAGGT 92
||: ||: || || ||||| || ||||| |||
Db 46 CAGRYTGYTGACGTGGACCTCCTGATAAGATTAGAT 9

RESULT 14

AX159152
LOCUS AX159152 50 bp DNA linear PAT 22-
JUN-2001
DEFINITION Sequence 2480 from Patent WO0140521.
ACCESSION AX159152
VERSION AX159152.1 GI:14540483
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shimketa,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0140521-A 2480 07-JUN-2001;
Curagen Corporation (US)
FEATURES Location/Qualifiers
source 1..50
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 25..26
/note="Nucleotide deleted between bases 25 and 26
Accession number cg39667412"
misc_feature 26
/note="2 of 2 allelic variants (2479 is other entry)"

ORIGIN

Query Match 17.6%; Score 16.4; DB 6; Length 50;
Best Local Similarity 61.9%; Pred. No. 3.2e+05;
Matches 26; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy 37 CCTTGGTTTCAACACTATCGGAATGTGACTGTGGGCTTCCA 78
|| ||| || ||||| || ||||| ||| |||
Db 9 CCATGGCGTGACACAAAGGGGACTGTCAATCACAGGCTTTCA 50

RESULT 15

AR078049/c
LOCUS AR078049 40 bp DNA linear PAT 31-
AUG-2000
DEFINITION Sequence 103 from patent US 5962272.
ACCESSION AR078049
VERSION AR078049.1 GI:10004795